

241421.txt
SEQUENCE LISTING

<110> Sewalt, Vincent
Hastings, Craig
Meeley, Robert
Hantke, Sabine
Jung, Rudolf
Everard, John
Allen, Stephen

<120> COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF
PROTEINS

<130> 5718-119 (035718/241421)

<150> 60/250,703

<151> 2000-12-01

<160> 25

<170> PatentIn version 3.0

<210> 1

<211> 797

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (187)..(573)

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120

cgctactccg ctccccctca gtcctcagtt cctcacctag cggtagcgtg cgcgcgggag
180

acgtag atg gcg gct tcg gag gcg gca gcg gcg gcg gca aca ccg gtg
228

Met	Ala	Ala	Ser	Glu	Ala	Ala	Ala	Ala	Ala	Thr	Pro	Val
1				5					10			

acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg
276

Thr	Pro	Thr	Glu	Gly	Thr	Val	Ile	Ala	Ile	His	Ser	Leu	Glu	Glu	Trp
15					20				25				30		

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att
324

Ser	Ile	Gln	Ile	Glu	Glu	Ala	Asn	Ser	Ala	Lys	Lys	Leu	Val	Val	Ile
				35				40					45		

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att
372

Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile

50

55

60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt
420

Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
65 70 75

gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc
468

Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
516

Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
564

Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
115 120 125

gcc tcg tag atcagtgatg ccgtaatgta gtattcgcct aaataagagg

613

Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
673

tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc
733

tgcttggtgct tttcatacca tgtttgctct ttcagctgag gtgttaaaaa aaaaaaaaaa
793

aaaa

797

<210> 2

<211> 128

<212> PRT

<213> Zea mays

<400> 2

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1 5 10 15

Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
35 40 45

[illegible]

THE

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350
Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
398
Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
446
Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
115 120 125

gcc tcg tag atcagtgatg ccgtaatgta gtattcgcct aaataagagg
495
Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
555

tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc
615

tgcttggtgct ttccatacca tgtttgctct ttcagctgag gtgttatatcg gtaaactcgga
675

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795

aaaa
799

<210> 4
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<213> Zea mays

<400> 4

Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val Ala Pro
1 5 10 15

Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
35 40 45

Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
50 55 60

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Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
65 70 75 80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
85 90 95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
100 105 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
115 120 125

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<213> Zea mays

<220>
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<222> (3)..(194)

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47
Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu
1 5 10 15

gcg gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gta
95
Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val
20 25 30

ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag
143
Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys
35 40 45

gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tcg
191
Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
50 55 60

taa actcctgtgg ttgcgctggg acggagttgc tgaagtgaaa tggtccttc
244

tctcaatgct gaaaaaaggg ggaaaaacta tgtgaaaatg atggtagacg tgtctgggtc
304

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364

aaa
367

<210> 6
 <211> 63
 <212> PRT
 <213> Zea mays

<400> 6

Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu Ala
 1 5 10 15

Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
 20 25 30

Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys Asp
 35 40 45

Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
 50 55 60

<210> 7
 <211> 720
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (38)..(442)

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 55

Met Gly Ser Phe Phe Ser
 1 5

acc tta gtg acg ccc cct ccg ccc gcc gcc gac gac ccg aac tgc gcc
 103

Thr Leu Val Thr Pro Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala
 10 15 20

gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc
 151

Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala
 25 30 35

cac aag agc agc agc aag ctg atg gtg atc gac ttc tcg gcg tcc tgg
 199

His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp
 40 45 50

tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc
 247

Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser
 55 60 65 70

cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctc gcg
295

Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala
75 80 85

gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg
343

Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
90 95 100

gtc aag gat ggg aag gag gta ggc cgt gtg att ggg gct aag aag gac
391

Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp
105 110 115

gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc
439

Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser Ser
120 125 130

taa cttagcagtg catacactcc caccttatta ctggtttctc gactccagtg
492

gttcgcctgg gacgggggtg ctgaaatggt tcccttctct gaatactgaa aaatcaaaaa
552

aagaagtata tgaaaaaatg atggtagacg tgtctgggtc aataagagtt tctgaaactt
612

ggatttgtat gtgtcagtct ctgtgttctg tttccaagga atggatcatg tgagtttgga
672

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720

<210> 8

<211> 134

<212> PRT

<213> Zea mays

<400> 8

Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala
1 5 10 15

Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr
20 25 30

Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile
35 40 45

Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala
50 55 60

Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val
65 70 75 80

Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala
85 90 95

Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val
100 105 110

Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val
115 120 125

Thr Ser Ser Ser Ser Ser
130

<210> 9
<211> 722
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (84)..(455)

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113

Met Ala Ser Glu Glu Glu Gly Val Val Ile
1 5 10

gcc tgc cac acc aag gcc gac ttc gac gcc cac atg gcc aag gcc aag
161

Ala Cys His Thr Lys Ala Asp Phe Asp Ala His Met Ala Lys Ala Lys
15 20 25

gag gcc ggc aag ctg gtg atc att gac ttc acg gcc tcc tgg tgc ggc
209

Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly
30 35 40

ccc tgc cgc ttc atc gcg cca ctg ttc gtc gag cac gcc aag aag ttc
257

Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe
45 50 55

acc cag gct gtg ttc ctg aag gtg gac gtg gac gag ctg aag gaa gtt
305

Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Glu Val
60 65 70

gcc gcg gcc tac gat gtc gag gcg atg ccg acc ttc cac ttc gtc aag
353
Ala Ala Ala Tyr Asp Val Glu Ala Met Pro Thr Phe His Phe Val Lys
75 80 85 90

aac ggg gtg acg gtc gag acc gtc gtc ggt gcc agg aag gag aac ctc
401
Asn Gly Val Thr Val Glu Thr Val Val Gly Ala Arg Lys Glu Asn Leu
95 100 105

ctg gcc cag atc gag aag cac tgc gcc gcg gcc gtg cct gct gcg tct
449
Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala Val Pro Ala Ala Ser
110 115 120

gcg tag agaggatgga ccagcacgtg gcggtggcgg tggcggttgt cttgtcgttt
505
Ala

tcagtttggg cttgtcagct gtggctgggt ggttgattgt gaactggagc atgcagtttt
565

actctgggag cccatcattt gggtggctca ggtgtcaata atctgtatac cttaatcatg
625

gatagttggt gtgagttgtg attggacttt ggaatttgga tgtctggctt cgttctgtta
685

tgatgatgat gatggattga aaaaaaaaaa aaaaaaa
722

<210> 10
<211> 123
<212> PRT
<213> Zea mays

<400> 10

Met Ala Ser Glu Glu Glu Gly Val Val Ile Ala Cys His Thr Lys Ala
1 5 10 15

Asp Phe Asp Ala His Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val
20 25 30

Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala
35 40 45

Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu
50 55 60

Lys Val Asp Val Asp Glu Leu Lys Glu Val Ala Ala Ala Tyr Asp Val
65 70 75 80


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                                241421.txt
                                100
                                105
95
gcc cag atc gag aag cat gcc gcg cct gcg cct gcg tct gcg tct gcc
449
Ala Gln Ile Glu Lys His Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
110 115 120

taa aggagatcag atcagtcgtc gccgtcaata agggccagca cgtatggctg
502

taaatgttgt cgttatcagt tctggctttg tcgtttgttg gcgattgtga actagtagta
562

tgtttgtttc tatccgagcc ggaggcgata cttaaccatg gatacttggt gtgagttcgt
622

ttctgttcgc gtgtgactct tgaattgaat caaccagctc accactgcac caggccgtgg
682

tgagtgtga cagtgatttc ctgttaaaaa aaaaaaaaaa aaaaa
727

<210> 12
<211> 122
<212> PRT
<213> Zea mays

<400> 12

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Lys Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala

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120

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<400> 13
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Met Ala Ala Glu Glu
1 5

ggt gcc gtg atc gcg tgc cac acc aag gac gag ttc gac gcc cgc atg
103

Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu Phe Asp Ala Arg Met
10 15 20

gcc aag gcc aag gag cag ggc aag ctg gtg gtc atc gac ttc atg gcc
151

Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val Ile Asp Phe Met Ala
25 30 35

ccc tgg tgc agt ggg tgc cag atg atg gcc ccg gtg tac gcg gac tgc
199

Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro Val Tyr Ala Asp Cys
40 45 50

gcc agc aag tac cct tcc gcg gtc ttc ctc gag gtc gac gtc gac gaa
247

Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu Val Asp Val Asp Glu
55 60 65

ctg ctg gaa gtc gcg aag atc tac ggc gtc cat gtg atg ccg acc ttc
295

Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His Val Met Pro Thr Phe
70 75 80 85

tgc ttc atc agg aac ggc gag acg ctc gag agc ttt gct acc gtc gac
343

Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser Phe Ala Thr Val Asp
90 95 100

gag gac gag ctc cgg gac gcc gtc agg aag tac gcc gcc gct ggc act
391

Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr Ala Ala Ala Gly Thr
105 110 115

acg acg gct cct gcc tcg gcg tcc gcc taa ttcaggagat gtgatgtgta
441

Thr Thr Ala Pro Ala Ser Ala Ser Ala
120 125

gcaaatagcg cgcgcgcacc agtcgtcaat aaataaataa ataaataaat aaataaataa

ataaataaat aaaggccaac gtacgacgac aaattagtgg cgcgcgcggt agtagctagc
561

agagtatgcg cggccactgt gtcgatctgc agtttggtcg tttaaaagtg attgtagtgt
621

gtactatggt cagctcgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
681

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aaaaaaaaaa aaaaaaaaaa
700
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<210>	14
<211>	126
<212>	PRT
<213>	Zea mays

<400> 14

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1 5 10 15

Phe Asp Ala Arg Met Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Met Ala Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro
35 40 45

Val Tyr Ala Asp Cys Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu
50 55 60

Val Asp Val Asp Glu Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His
65 70 75 80

Val Met Pro Thr Phe Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser
85 90 95

Phe Ala Thr Val Asp Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr
100 105 110

Ala Ala Ala Gly Thr Thr Thr Ala Pro Ala Ser Ala Ser Ala
115 120 125

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<210> 15
<211> 658
<212> DNA
<213> Hordeum vulgare
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<220>

<221> CDS

<222> (52)..(420)

<400> 15

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57

Met Ala
1

gcg tcg gca acg gcg gcg gca gtg gcg gcg gag gtg atc tcg gtc cac
105

Ala Ser Ala Thr Ala Ala Ala Val Ala Ala Glu Val Ile Ser Val His
5 10 15

agc ctg gag cag tgg acc atg cag atc gag gag gcc aac acc gcc aag
153

Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr Ala Lys
20 25 30

aag ctg gtg gtg att gac ttc act gca tca tgg tgc gga cca tgc cgc
201

Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg
35 40 45 50

atc atg gct cca gtt ttc gct gat ctc gcc aag aag ttc cca aat gct
249

Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro Asn Ala
55 60 65

gtt ttc ctc aag gtc gac gtg gat gaa ctg aag ccc att gct gag caa
297

Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala Glu Gln
70 75 80

ttc agt gtc gag gcc atg cca acg ttc ctg ttc atg aag gaa gga gac
345

Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu Gly Asp
85 90 95

gtc aag gac agg gtt gtc gga gct atc aag gag gaa ctg acc gcc aag
393

Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr Ala Lys
100 105 110

gtt ggg ctt cac gcg gcg gcc cag taa ttacctattg gtgtagtatt
440

Val Gly Leu His Ala Ala Ala Gln
115 120

cgcttaaata aaattgccgc tcaagaagac tatgaatgct gtgtactgct tgctacttgt
500

tggttggttta tggatactgc gatgcttgat ccaagctagt gtgcttttgc atatggttaa
560

ccaaaacagg attgctaaat cttagtcgac tgagatttaa ccaagtctta gtcaaagcta
620

241421.txt
tattggcgtg atcttacgta aaaaaaaaaa aaaaaaaa
658

<210> 16
<211> 122
<212> PRT
<213> Hordeum vulgare

<400> 16

Met Ala Ala Ser Ala Thr Ala Ala Ala Val Ala Ala Glu Val Ile Ser
1 5 10 15

Val His Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr
20 25 30

Ala Lys Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro
35 40 45

Cys Arg Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro
50 55 60

Asn Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala
65 70 75 80

Glu Gln Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu
85 90 95

Gly Asp Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr
100 105 110

Ala Lys Val Gly Leu His Ala Ala Ala Gln
115 120

<210> 17
<211> 580
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<223> "n" at position 116, 118, 120, 125, 127, 317, 331, 434, 473,
482,
486, 493, 501, 507, 515, 519, 532, 542, and 579 can be an a, c,
g, or t

<400> 17
tcggatccca caccgaggaa aaggagaaga gagcgagggt cggaataatg gcggccgagg
60

"645000" 645000

agggtgccgt gatcgcgctgc cacaccaagg acgagttcga cgcccgcgatg gccaanngcn
120

aggannggc aagctggtgg tcatcgactt catggccccc tggcgagtg ggtgccagat
180

gatggccccc gtgtacgcgg actgcgccag caagtaccct tccgcggtct tcctcgaggt
240

cgacgtggac gaactgctgg aagtcgcgaa gatctacggc gtccatgtga tgccgacctt
300

ctgcttcac aggaacngcg agacgctcga nagctttgct accgtcgacg aagacgagct
360

ccgggacgcc gtcaggaagt acgcccgcgc tggcactacg acgtcctgc ctcggcgctc
420

gcctaattca gganatgtga tgtgtagcaa atagcgcgcg cgcacccatcg tcnataaata
480

antaantaat aantaattaa ntaantnaag ggccncgtnc aacaacaatt tntggccccg
540

cngtattact acaaatttgc cccccctgtt tcattctgcnt
580

<210> 18
<211> 590
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (60)..(425)

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,
g,
or t

<400> 18
gttgcaatna caacgaacag aagctctcga tctcaccgac accgaggaag aagagatca
59

atg gcg tcc gag cag gga gtc gtg atc gcg tgc cac agc aag gct gag
107
Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

ttc gac gcc cac atg acc aag gcc cag gaa gcc ggc aag ctg gtg gtc
155
Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

241421.txt

atc gac ttc act gcc gcc tgg tgc ggt cca tgc cgc gcc atc gcc cca
203
Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

ctg ttc gtc gaa cac gcc aag aag ttc act cag gtc gtc ttc ctg aag
251
Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

gtg gac gtg gac gaa gtg aag gaa gtc acc gcg gcc tac gag gtc gag
299
Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

gcg atg ccg acc ttc cac ttc gtc aag aac ggc aag acg gtc gcg acc
347
Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

atc gtg ggt gcc agg aag gac gag ctc ctg gcc cag atc gag aag cat
395
Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

gcc gcg cct gcg cct gcg tct gcg tct gcc taaaggagat cagtcgtcgc
445
Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

cgtcaataag ggccagcacg tatggctgta aatgttgctg ttatcagntc tggctttgtc
505

gtttgtgggc gattgtgaac tagtagtatg tnggttctat ccnaagccgg aggcgatctt
565

aacctgggat acttgntgng aaaaa
590

<210> 19
<211> 122
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,
g,
or t

<400> 19

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

<210> 20
<211> 948
<212> DNA
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<220>
<221> CDS
<222> (3)..(737)

<400> 20
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47
Lys Ile Leu Thr Glu Thr Val Thr Thr Val Asp Phe Ser Ala Arg
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95
Pro Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val
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143
Val Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser
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Asp Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly
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Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly

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70

75

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287

Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln
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Val Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met
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Gln Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser
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431

Glu Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly
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479

Val Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val
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527

Ala Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu
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575

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623

Gly Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val
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671

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210 215 220

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719

Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln
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767

Glu Gly Lys Thr Asp
240

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948

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Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser Asp
35 40 45

Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala
50 55 60

Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly Asp
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Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln Val
85 90 95

Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met Gln
100 105 110

Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser Glu
115 120 125

Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val
130 135 140

Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala
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Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly

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96
Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
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atc ggt cac gag ccg gcg aca aaa ttt ctt gga ggg cag ctc gag ctc
144
Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
35 40 45

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192
Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
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gtg cag ggg gtc ttt gca gct ggg gat gtc cag gac aag aag tac cgc
240
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288

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 336

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 35 40 45

Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
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Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
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 162

Leu Arg Thr Arg Ile Cys Ile Ile Gly Ser Gly Pro Ala Ala His Thr
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Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Val Leu Phe Glu
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Gly Trp Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr
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 306

Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala
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Asp Leu Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn
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Ile Leu Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe
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Arg Val Ser Ala Asp Ser Thr Thr Val Leu Ala Asp Ala Val Ile Val
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140

145

150

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786

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978

Thr His Thr Ser Val Lys Gly Val Phe Ala Ala Gly Asp Val Gln Asp
285 290 295

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1074

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241421.txt

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